

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Fukudome, Kenji  
Esmon, Charles T.

(ii) TITLE OF INVENTION: Cloning and Regulation of an Endothelial  
Cell Protein C/Activated Protein C Receptor

(iii) NUMBER OF SEQUENCES: 6

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Patrea L. Pabst  
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Street  
(C) CITY: Atlanta  
(D) STATE: Georgia  
(E) COUNTRY: US  
(F) ZIP: 30306-3450

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/289,699  
(B) FILING DATE: 12-AUG-1994  
(C) CLASSIFICATION: 530

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Pabst, Patrea L.  
(B) REGISTRATION NUMBER: 31,284  
(C) REFERENCE/DOCKET NUMBER: OMRF152

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (404) 873-8794  
(B) TELEFAX: (404) 873-8795

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1302 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..1302

(D) OTHER INFORMATION: /note= "Nucleotides 25 through 738 encode the

Endothelial Cell Protein Receptor of Sequence ID No. 2."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGGTCCGGA GCCTCAACTT CAGGATGTTG ACAACATTGC TGCCGATACT GCTGCTGTCT 60  
GGCTGGGCCT TTTGTAGCCA AGACGCCTCA GATGGCCTCC AAAGACTTCA TATGCTCCAG 120  
ATCTCCTACT TCCGCGACCC CTATCACGTG TGGTACCAGG GCAACGCGTC GCTGGGGGGA 180  
CACCTAACGC ACGTGCTGGA AGGCCCAGAC ACCAACACCA CGATCATTCA GCTGCAGCCC 240  
TTGCAGGAGC CCGAGAGCTG GGCGCGCAGC CAGAGTGGCC TGCAGTCCTA CCTGCTCCAG 300  
TTCCACGGCC TCGTGCGCCT GGTGCACCAG GAGCGGACCT TGGCCTTTCC TCTGACCATC 360  
CGCTGCTTCC TGGGCTGTGA GCTGCCTCCC GAGGGCTCTA GAGCCCATGT CTTCTTCGAA 420  
GTGGCTGTGA ATGGGAGCTC CTTTGTGAGT TTCCGGCCCG AGAGAGCCTT GTGGCAGGCA 480  
GACACCCAGG TCACCTCCGG AGTGGTCACC TTCACCCTGC AGCAGCTCAA TGCCTACAAC 540  
CGCACTCGGT ATGAACTGCG GGAATTCCTG GAGGACACCT GTGTGCAGTA TGTGCAGAAA 600  
CATATTTCCG CGGAAAACAC GAAAGGGAGC CAAACAAGCC GCTCCTACAC TTCGCTGGTC 660  
CTGGGCGTCC TGGTGGGCGG TTTCATCATT GCTGGTGTGG CTGTAGGCAT CTTCTGTGTC 720  
ACAGGTGGAC GGCGATGTTA ATTACTCTCC AGCCCCGTCA GAAGGGGCTG GATTGATGGA 780  
GGCTGGCAAG GGAAAGTTTC AGCTCACTGT GAAGCCAGAC TCCCCAACTG AAACACCAGA 840  
AGGTTTGGAG TGACAGCTCC TTTCTTCTCC CACATCTGCC CACTGAAGAT TTGAGGGAGG 900  
GGAGATGGAG AGGAGAGGTG GACAAAGTAC TTGGTTTGCT AAGAACCTAA GAACGTGTAT 960  
GCTTTGCTGA ATTAGTCTGA TAAGTGAATG TTTATCTATC TTTGTGAAA ACAGATAATG 1020  
GAGTTGGGGC AGGAAGCCTA TGCGCCATCC TCCAAAGACA GACAGAATCA CCTGAGGCGT 1080  
TCAAAAGATA TAACCAATA AACAGTCAT CCACAATCAA AATACAACAT TCAATACTTC 1140  
CAGGTGTGTC AGACTTGGGA TGGGACGCTG ATATAATAGG GTAGAAAGAA GTAACACGAA 1200  
GAAGTGGTGG AAATGTAAAA TCCAAGTCAT ATGGCAGTGA TCAATTATTA ATCAATTAAT 1260  
AATATTAATA AATTTCTTAT ATTTAAAAA AAAAAAAAAA AA 1302

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..365

(D) OTHER INFORMATION: /note= "Endothelial Cell Protein Receptor encoded by nucleotides 1 through 1302 of Sequence ID No. 1."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1..15

(D) OTHER INFORMATION: /note= "Amino acids 1-15 represent a putative signal sequence."

(ix) FEATURE:

(A) NAME/KEY: Domain

(B) LOCATION: 211..236

(D) OTHER INFORMATION: /note= "Amino acids 211-236 represent a putative transmembrane domain."

(ix) FEATURE:

(A) NAME/KEY: Active-site

(B) LOCATION: 47..174

(D) OTHER INFORMATION: /note= "Amino acids 47-49, 64-66, 136-138 and 172-174 represent potential N-glycosylation sites."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 17..186

(D) OTHER INFORMATION: /note= "Amino acids 17, 114, 118 and 186 represent extracellular cysteine residues."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Thr Thr Leu Leu Pro Ile Leu Leu Leu Ser Gly Trp Ala Phe  
1 5 10 15

Cys Ser Gln Asp Ala Ser Asp Gly Leu Gln Arg Leu His Met Leu Gln  
20 25 30

Ile Ser Tyr Phe Arg Asp Pro Tyr His Val Trp Tyr Gln Gly Asn Ala  
35 40 45

Ser Leu Gly Gly His Leu Thr His Val Leu Glu Gly Pro Asp Thr Asn  
50 55 60

Thr Thr Ile Ile Gln Leu Gln Pro Leu Gln Glu Pro Glu Ser Trp Ala  
65 70 75 80

Arg Thr Gln Ser Gly Leu Gln Ser Tyr Leu Leu Gln Phe His Gly Leu  
85 90 95

Val Arg Leu Val His Gln Glu Arg Thr Leu Ala Phe Pro Leu Thr Ile  
 100 105 110  
 Arg Cys Phe Leu Gly Cys Glu Leu Pro Pro Glu Gly Ser Arg Ala His  
 115 120 125  
 Val Phe Phe Glu Val Ala Val Asn Gly Ser Ser Phe Val Ser Phe Arg  
 130 135 140  
 Pro Glu Arg Ala Leu Trp Gln Ala Asp Thr Gln Val Thr Ser Gly Val  
 145 150 155 160  
 Val Thr Phe Thr Leu Gln Gln Leu Asn Ala Tyr Asn Arg Thr Arg Tyr  
 165 170 175  
 Glu Leu Arg Glu Phe Leu Glu Asp Thr Cys Val Gln Tyr Val Gln Lys  
 180 185 190  
 His Ile Ser Ala Glu Asn Thr Lys Gly Ser Gln Thr Ser Arg Ser Tyr  
 195 200 205  
 Thr Ser Leu Val Leu Gly Val Leu Val Gly Gly Phe Ile Ile Ala Gly  
 210 215 220  
 Val Ala Val Gly Ile Phe Leu Cys Thr Gly Gly Arg Arg Cys  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Leu Thr Lys Phe Leu Leu Leu Leu Leu Leu Leu Pro Gly Cys  
 1 5 10 15  
 Ala Phe Val Thr Pro Met Ala Pro Lys Ala Ala Tyr Ala Pro Asp Leu  
 20 25 30  
 Leu Phe Pro Arg Pro Pro Ser Cys Glu Ala Ser Gly Gln Arg Ser Leu  
 35 40 45  
 Gly Lys Leu Leu Thr His Thr Leu Glu Gly Pro Ser Gln Asn Val Thr  
 50 55 60  
 Ile Leu Gln Leu Gln Pro Trp Gln Asp Pro Glu Ser Trp Glu Arg Thr  
 65 70 75 80

Glu Ser Gly Leu Gln Ile Tyr Leu Thr Gln Phe Glu Ser Leu Val Lys  
                     85                    90                    95  
 Leu Val Tyr Arg Glu Arg Lys Glu Asn Val Phe Phe Pro Leu Thr Val  
                     100                    105                    110  
 Ser Cys Ser Leu Gly Cys Glu Leu Pro Glu Glu Glu Glu Glu Gly Ser  
                     115                    120                    125  
 Glu Pro His Val Phe Phe Asp Val Ala Val Asn Gly Ser Ala Phe Val  
                     130                    135                    140  
 Ser Phe Arg Pro Lys Thr Ala Val Trp Val Ser Gly Ser Gln Glu Pro  
                     145                    150                    155                    160  
 Ser Lys Ala Ala Asn Phe Thr Leu Lys Gln Leu Asn Ala Tyr Asn Arg  
                     165                    170                    175  
 Thr Arg Tyr Glu Leu Gln Glu Phe Leu Gln Asp Thr Cys Val Glu Phe  
                     180                    185                    190  
 Leu Glu Asn His Ile Thr Thr Gln Asn Met Lys Gly Ser Gln Thr Gly  
                     195                    200                    205  
 Arg Ser Tyr Thr Ser Leu Val Leu Gly Ile Leu Met Gly Cys Phe Ile  
                     210                    215                    220  
 Ile Ala Gly Val Ala Val Gly Ile Phe Met Cys Thr Ser Gly Arg Gly  
                     225                    230                    235                    240  
 Leu Leu Ile Ile

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp  
 1                    5                    10                    15  
 Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln  
                     20                    25                    30  
 Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala  
                     35                    40                    45  
 Trp Leu Gly Glu Leu Gln Thr His Ser Trp Ser Asn Asp Ser Asp Thr

50	55	60
Val Arg Ser Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln		
65	70	75 80
Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr		
	85	90 95
Arg Asp Val Lys Glu Phe Ala Lys Met Leu Arg Leu Ser Tyr Pro Leu		
	100	105 110
Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala Ser		
	115	120 125
Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe		
	130	135 140
Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val Asn		
	145	150 155 160
Leu Ala Ile Gln Val Leu Asn Gln Asp Lys Trp Thr Arg Glu Thr Val		
	165	170 175
Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu		
	180	185 190
Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala Trp		
	195	200 205
Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Val Cys		
	210	215 220
His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met Arg		
	225	230 235 240
Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn		
	245	250 255
Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala Gly		
	260	265 270
Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly		
	275	280 285
Gln Asp Ile Val Leu Tyr Trp Gly Gly Ser Tyr Thr Ser Met Gly Leu		
	290	295 300
Ile Ala Leu Ala Val Leu Ala Cys Leu Leu Phe Leu Leu Ile Val Gly		
	305	310 315 320
Phe Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Gly Val Leu		
	325	330 335

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Arg	Tyr	Leu	Pro	Cys	Leu	Leu	Leu	Trp	Ala	Phe	Leu	Gln	Val	Trp	
1				5					10					15		
Gly	Gln	Ser	Glu	Val	Gln	Gln	Lys	Asn	Tyr	Thr	Phe	Arg	Cys	Leu	Gln	
			20					25					30			
Thr	Ser	Ser	Phe	Ala	Asn	Ile	Ser	Trp	Ser	Arg	Thr	Asp	Ser	Leu	Ile	
		35					40					45				
Leu	Leu	Gly	Asp	Leu	Gln	Thr	His	Arg	Trp	Ser	Asn	Asp	Ser	Ala	Thr	
	50					55					60					
Ile	Ser	Phe	Thr	Lys	Pro	Trp	Ser	Gln	Gly	Lys	Leu	Ser	Asn	Gln	Gln	
65					70					75					80	
Trp	Glu	Lys	Leu	Gln	His	Met	Phe	Gln	Val	Tyr	Arg	Val	Ser	Phe	Thr	
			85						90					95		
Arg	Asp	Ile	Gln	Glu	Leu	Val	Lys	Met	Met	Ser	Pro	Lys	Glu	Asp	Tyr	
			100					105						110		
Pro	Ile	Glu	Ile	Gln	Leu	Ser	Thr	Gly	Cys	Glu	Met	Tyr	Pro	Gly	Asn	
		115					120					125				
Ala	Ser	Glu	Ser	Phe	Phe	His	Val	Ala	Phe	Gln	Gly	Lys	Tyr	Ala	Val	
	130					135					140					
Arg	Phe	Arg	Gly	Thr	Ser	Trp	Gln	Arg	Val	Leu	Gly	Ala	Pro	Ser	Trp	
145					150					155					160	
Leu	Asp	Leu	Pro	Ile	Lys	Val	Leu	Asn	Ala	Asp	Gln	Gly	Thr	Ser	Ala	
			165					170						175		
Thr	Val	Gln	Thr	Leu	Leu	Asn	Asp	Thr	Trp	Pro	Gln	Phe	Ala	Arg	Gly	
		180						185					190			
Leu	Leu	Glu	Ala	Gly	Lys	Ser	Asp	Leu	Glu	Lys	Gln	Glu	Lys	Pro	Val	
	195						200					205				
Ala	Trp	Leu	Ser	Ser	Val	Pro	Ser	Ser	Ala	His	Gly	His	Leu	Gln	Leu	
	210					215					220					
Val	Cys	His	Val	Ser	Gly	Phe	Tyr	Pro	Lys	Pro	Val	Trp	Val	Met	Trp	
225					230					235					240	
Met	Arg	Gly	Asp	Gln	Glu	Gln	Gln	Gly	Thr	His	Arg	Gly	Asp	Phe	Leu	

				245					250						255				
Pro	Asn	Ala	Asp	Glu	Thr	Trp	Tyr	Leu	Gln	Ala	Thr	Leu	Asp	Val	Glu				
			260					265					270						
Ala	Gly	Glu	Glu	Ala	Gly	Leu	Ala	Cys	Arg	Val	Lys	His	Ser	Ser	Leu				
		275					280					285							
Gly	Gly	Gln	Asp	Ile	Ile	Leu	Tyr	Trp	Asp	Ala	Arg	Gln	Ala	Pro	Val				
	290					295					300								
Gly	Leu	Ile	Val	Phe	Ile	Val	Leu	Ile	Met	Leu	Val	Val	Val	Gly	Ala				
305					310					315					320				
Val	Val	Tyr	Tyr	Ile	Trp	Arg	Arg	Arg	Ser	Ala	Tyr	Gln	Asp	Ile	Arg				
				325					330					335					

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Leu	Thr	Lys	Phe	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Pro	Gly	Cys	
1				5				10					15		
Ala	Leu	Cys	Asn	Ser	Asp	Gly	Ser	Gln	Ser	Leu	His	Met	Leu	Gln	Ile
			20					25					30		
Ser	Tyr	Phe	Gln	Asp	His	His	His	Val	Arg	His	Gln	Gly	Asn	Ala	Ser
		35					40					45			
Leu	Gly	Lys	Leu	Leu	Thr	His	Thr	Leu	Glu	Gly	Pro	Ser	Gln	Asn	Val
	50					55					60				
Thr	Ile	Leu	Gln	Leu	Gln	Pro	Trp	Gln	Asp	Pro	Glu	Ser	Trp	Glu	Arg
65					70					75					80
Thr	Glu	Ser	Gly	Leu	Gln	Ile	Tyr	Leu	Thr	Gln	Phe	Glu	Ser	Leu	Val
				85					90					95	
Lys	Leu	Val	Tyr	Arg	Glu	Arg	Lys	Glu	Asn	Val	Phe	Phe	Pro	Leu	Thr
			100					105					110		
Val	Ser	Cys	Ser	Leu	Gly	Cys	Glu	Leu	Pro	Glu	Glu	Glu	Glu	Glu	Gly
		115					120					125			
Ser	Glu	Pro	His	Val	Phe	Phe	Asp	Val	Ala	Val	Asn	Gly	Ser	Ala	Phe



130 135 140  
Val Ser Phe Arg Pro Lys Thr Ala Val Trp Val Ser Gly Ser Gln Glu  
145 150 155 160  
Pro Ser Lys Ala Ala Asn Phe Thr Leu Lys Gln Leu Asn Ala Tyr Asn  
165 170 175  
Arg Thr Arg Tyr Glu Leu Gln Glu Phe Leu Gln Asp Thr Cys Val Glu  
180 185 190  
Phe Leu Glu Asn His Ile Thr Thr Gln Asn Met Lys Gly Ser Gln Thr  
195 200 205  
Gly Arg Ser Tyr Thr Ser Leu Val Leu Gly Ile Leu Met Gly Cys Phe  
210 215 220  
Ile Ile Ala Gly Val Ala Val Gly Ile Phe Met Cys Thr Ser Gly Arg  
225 230 235 240  
Arg Cys

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C1  
Cont